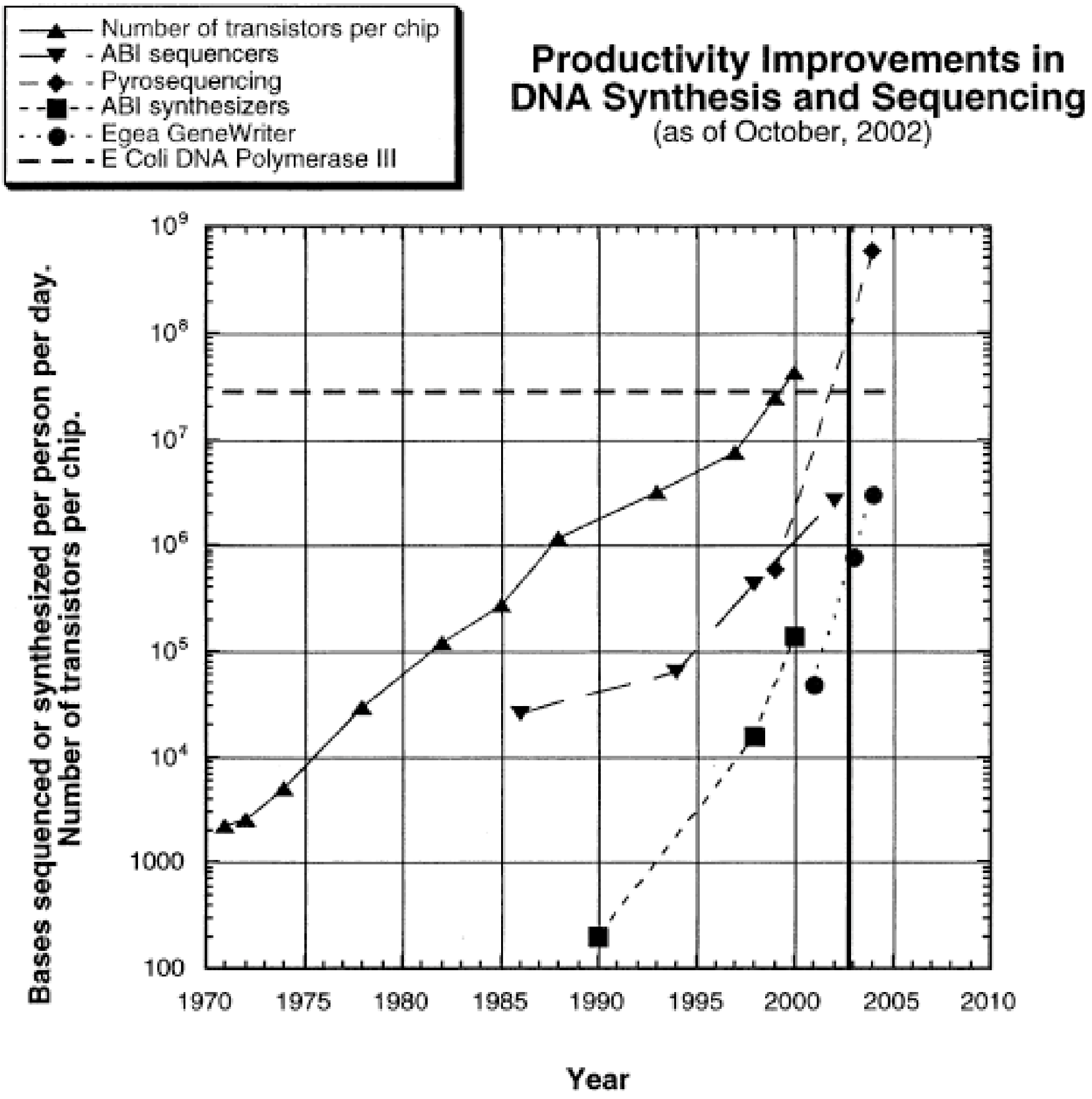
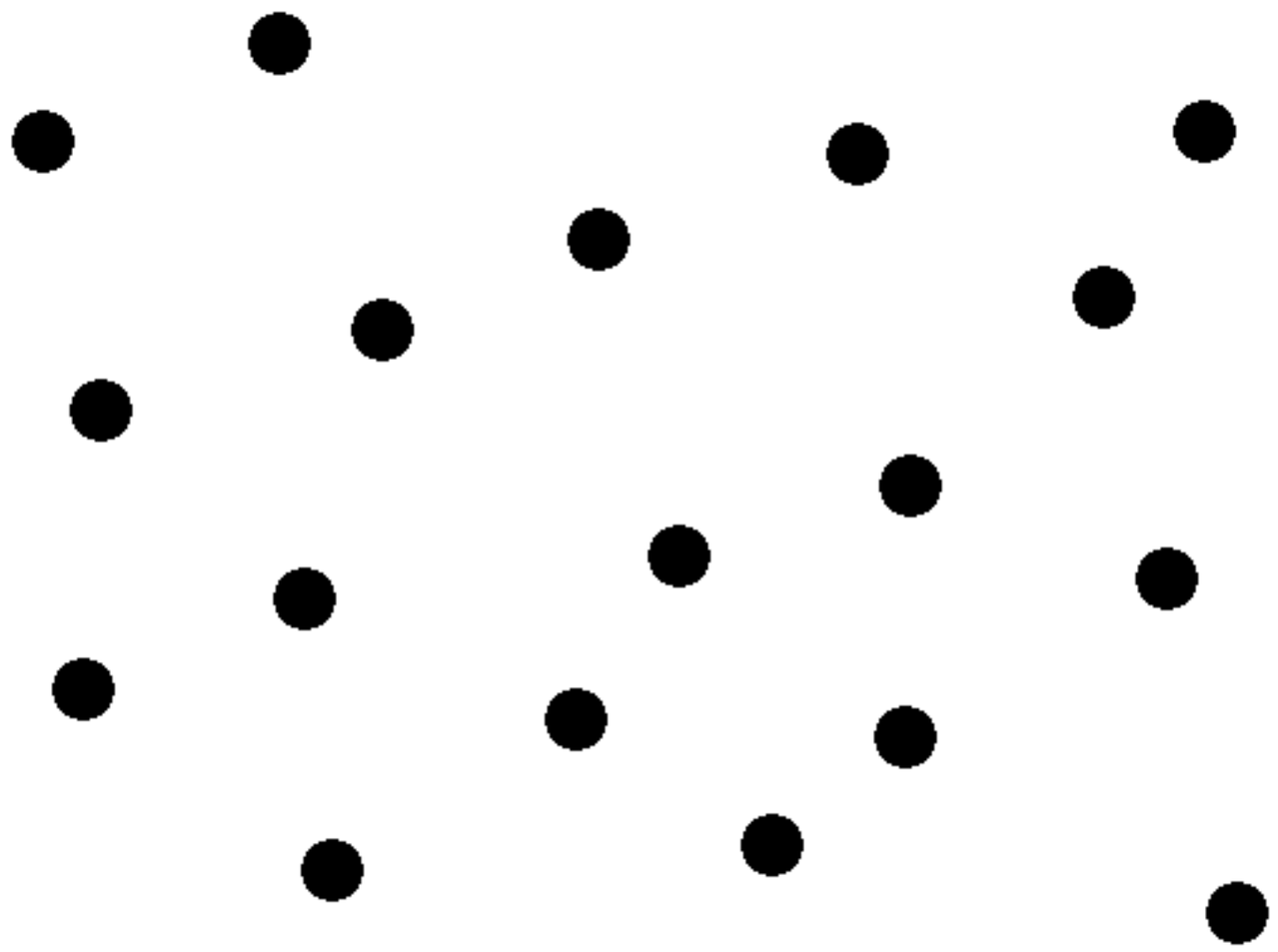

10-1030-55
dT
GLEN RESEARCH
0912014
5.0g
10-1010-15
dC
GLEN RESEARCH
0909030
10.0g
10-1020-55
dG
GLEN RESEARCH
0912013
5.0g
10-1000-15
dA
GLEN RESEARCH
0903052
10.0g



Carlson, Pace & Proliferation of Biological Technologies, Biosec. & Bioterror. 1(3):1 (2003)

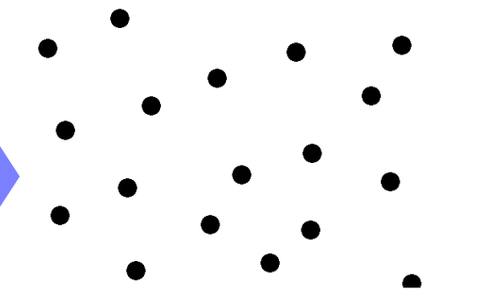


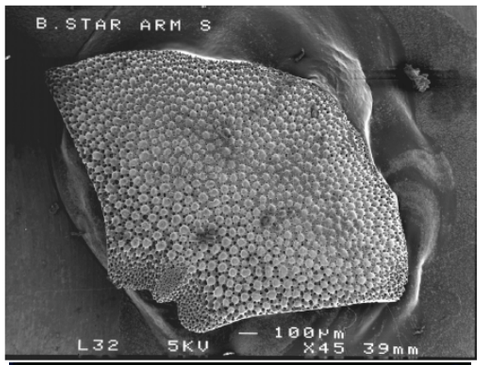
Struggle, limited success, struggle...

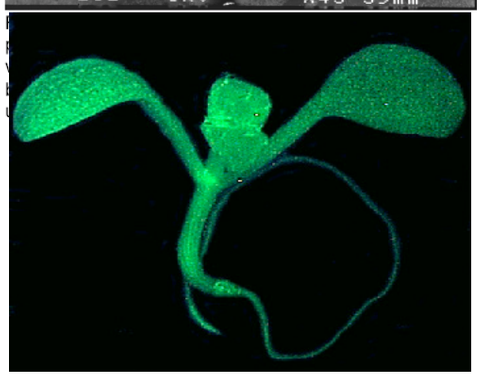
Design & Fabrication

Devices??

Systems??





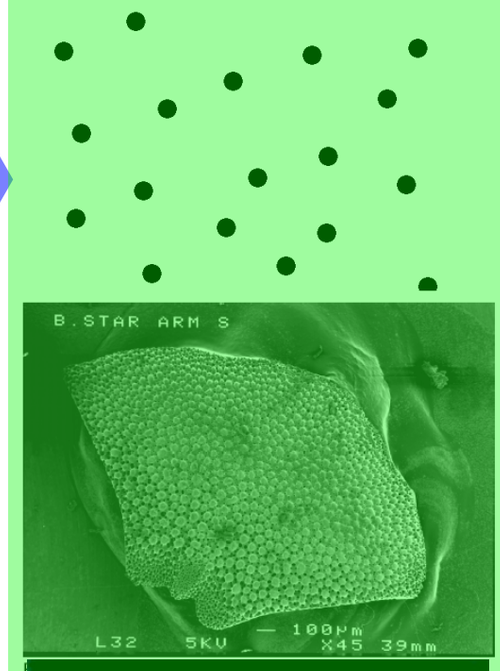


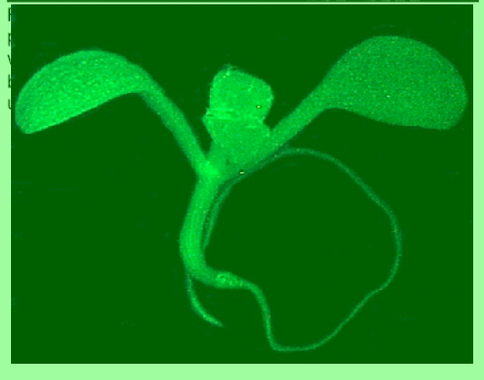
Struggle, success, reliable success

Design

Parts & Fabrication

Devices & Systems





Decoupling

Standardization

Abstraction

ON A SYSTEM OF

SCREW THREADS AND NUTS.

By WILLIAM SELLERS.

[Read before the FRANKLIN INSTITUTE, April 21, 1864.]

The importance of a uniform system of screw threads and nuts is so generally acknowledged by the engineering profession, that it needs no argument to set forth its advantages; and in offering any plan for their acceptance, it remains only to demonstrate its practicability and its superiority over any of the numerous special proportions now used by the different manufacturers. In this country no organized attempt has as yet been made to establish any system, each manufacturer having adopted whatever his judgment may have dictated as the best,

FIG. 2

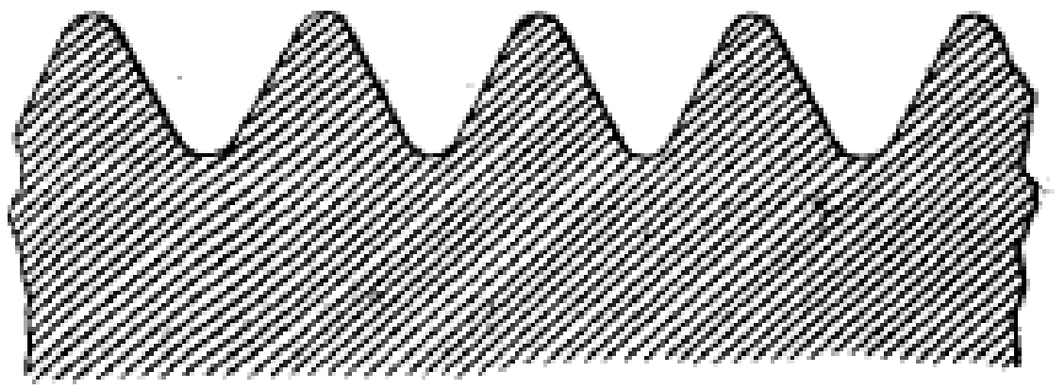
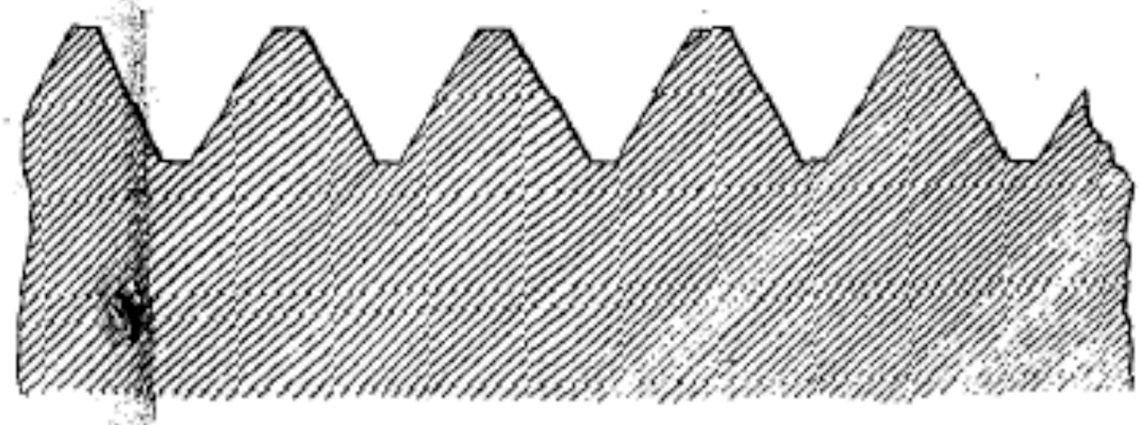


FIG. 6



```
--gca G  *AATTC GCGGCCGC T TCTAGA G--insert--T A   *CTAGA G---- 3'
--cgt CTTAA*  G CGCCGGCG A ACATCT C--insert--A TGATC*   T C---- 5'
      EcoRI       NotI       XbaI                    Mixed
```

```
5' --gca GAATTC GCGGCCGC T TCTAGA G --insert-- T ACTAGT A GCGGCCG CTGCAG gct--
   --cgt CTTAAG CGCCGGCG A ACATCT C ---------- A TGATCA T CGCCGGC GACGTC cga--
         EcoRI   NotI       XbaI                   SpeI     NotI    PstI
```

```
5' --T A  *CTAGA G --insert-- T ACTAGT A GCGGCCG CTGCA  *G gct-
3' --A TGATC*  T C --insert-- A TGATCA T CGCCGGC G*  ACGTC cga-
        Mixed                    SpeI     NotI      PstI
```

Note.
Parts and vectors must not contain bracketing sites.

Knight TF
Idempotent Vector Design for Standard Assembly of Biobricks.
MIT Synthetic Biology Working Group Communications (2003)

B0034-C0072-C0051-R0015-E2100

Registry of Standard Biological Parts

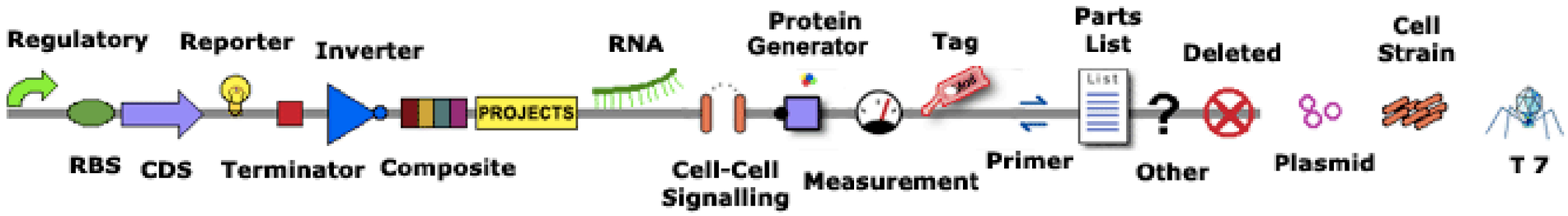
Massachusetts Institute of Technology

View Part

BBa_

Parts Catalog

Click on the icons below to see parts by category. more...



Web Site Update

Registry web site changes in support of iGEM 2005 are under way.
- The new account manager is in place with better support for groups, group leaders, and editing.
- Part categories are becoming more detailed, see the signalling category for an example.
- The new part viewer and editer is on the way soon.
- New Rolling Assembly tool under development.

Educational Programs

The Registry supports design classes where students make simple systems from standard, interchangeable biological parts and operate them in living cells.

Thirteen schools are participating in the **2005 Intercollegiate Genetically Engineered Machine** competition (**iGEM 2005**). The schools are: Berkeley, Caltech, Cambridge, Davidson, ETH Zurich, Harvard, MIT, Oklahoma, Penn State, Princeton, Toronto, UCSF, and UT Austin.

Employment

The Registry is looking for full-time Technical Assistants and Web Programmers. Please contact Staffing Services at MIT for details: Technical Assistant, Web Programmer.

Abstraction

Systems

Devices

Parts

DNA

Designs on life

Earlier this month, students from around the world locked horns in competition. Their challenge was to build functioning devices out of biological parts. **Erika Check** finds out how they got on.

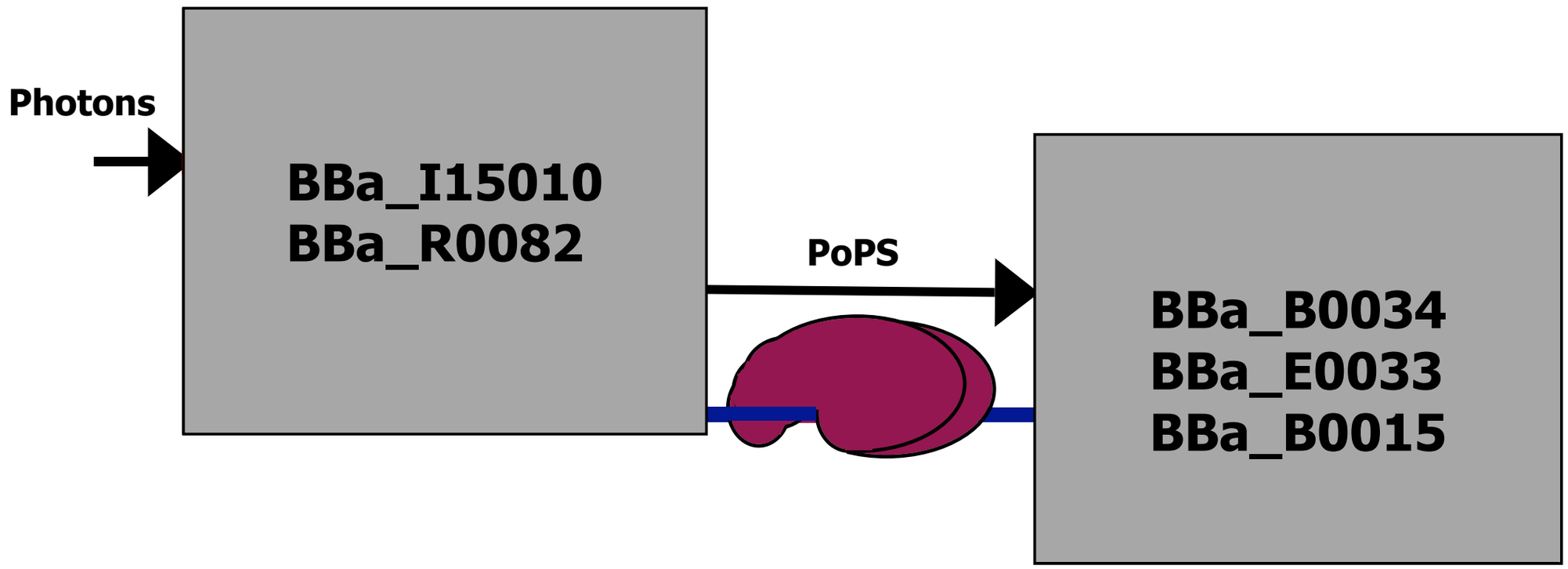
Even if you're thinking big, you usually have to start small. Especially, as a group of Swiss students found, when big means counting to infinity. The team was drawing up a blueprint for the world's first counting machine made entirely of biological parts. Although they had their sights on loftier numbers, they opted to go no higher than two. If the plan worked, it would be a proof-of-principle for a much larger tallying device.

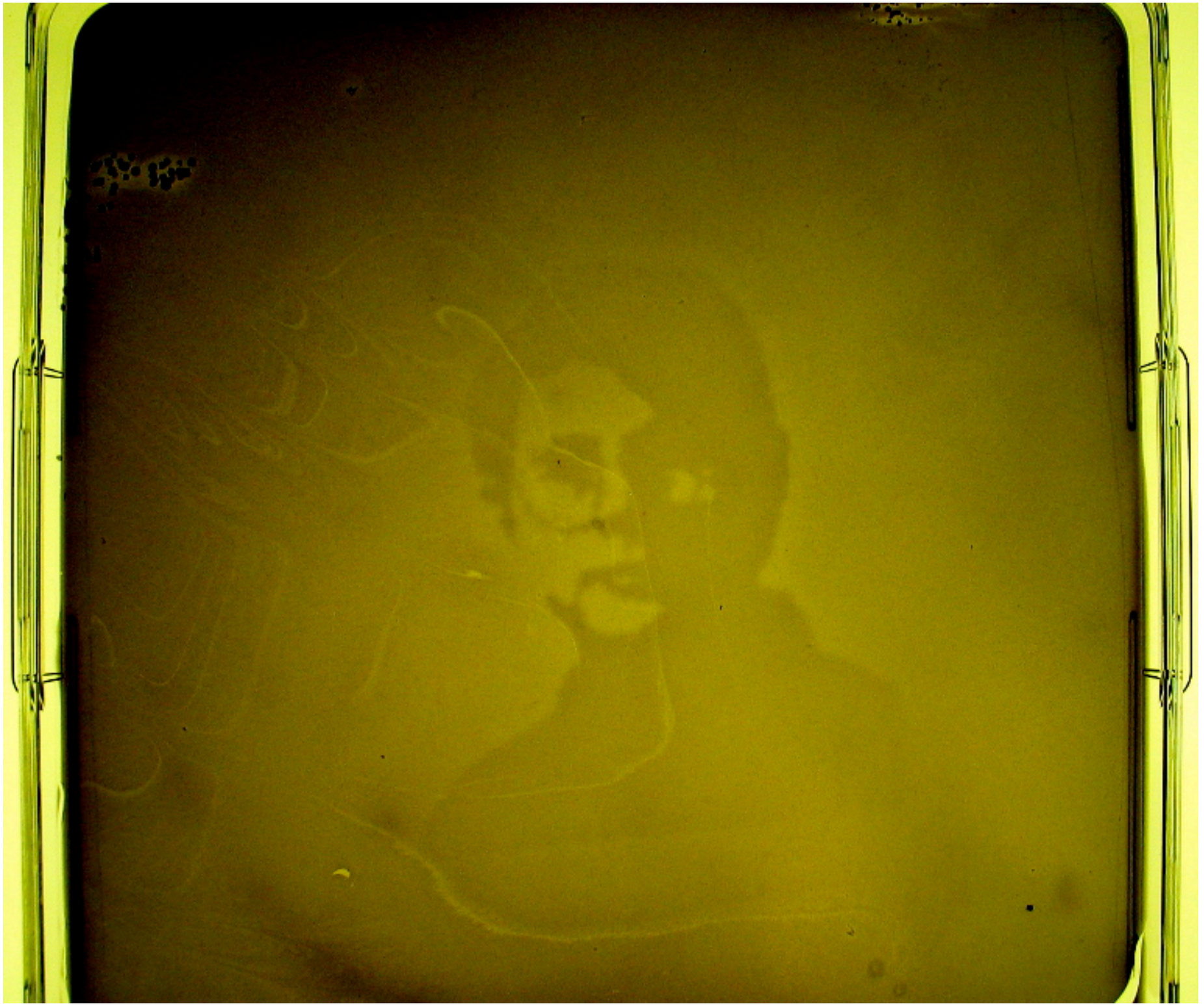
The group, from the Federal Institute of Technology (ETH) in Zurich, was one of 17 teams unveiling their projects at the first international Intercollegiate Genetically Engineered Machine (iGEM) competition, held at the Massachusetts Institute of Technology (MIT) in Cambridge on 5 and 6 November. The event attracted students from all over the world to design and build machines made entirely from biological components such as genes and proteins. They drew up grand designs for bacterial Etch-a-Sketches, photosensitive t-shirts, thermometers and sensors. And if none of the designs succeeded completely, that was more because of the limitations of the nascent science of synthetic biology than any lack of enthusiasm, creativity or hard work.

Synthetic biology aims to merge engineering approaches with biology. Researchers working at the most basic level are copying simple biological processes, such as the production of a protein from a gene. They break the process down into its component elements, such as a gene and the pieces of DNA

E. CHECK

Bidding for glory: teams from the ETH in Zurich (top), Cambridge, UK, (bottom right) and Massachusetts at the first international Intercollegiate Genetically Engineered Machine competition.


Photons
BBa_I15010
BBa_R0082
PoPS
BBa_B0034
BBa_E0033
BBa_B0015



Levskaya et al. (2005) Synthetic Biology: Engineering E.coli to see light. Nature 438, 441-442.

Molecular Systems Biology (2005) doi:10.1038/msb4100025

www.molecularsystemsbiology.com

molecular systems biology

Refactoring bacteriophage T7

Leon Y Chan[1,3], Sriram Kosuri[2,3] and Drew Endy[2,*]

[1] Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, USA and [2] Division of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA, USA
[3] These authors contributed equally to this work
* Corresponding author. Division of Biological Engineering, Massachusetts Institute of Technology, 68-580, 77 Massachusetts Avenue, Cambridge, MA 02139, USA. Tel.: +1 617 258 5152; Fax: +1 617 253 5865; E-mail: endy@mit.edu

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Natural biological systems are selected by evolution to continue to exist and evolve. Evolution likely gives rise to complicated systems that are difficult to understand and manipulate. Here, we redesign the genome of a natural biological system, bacteriophage T7, in order to specify an engineered surrogate that, if viable, would be easier to study and extend. Our initial design goals were to physically separate and enable unique manipulation of primary genetic elements. Implicit in our design are the hypotheses that overlapping genetic elements are, in aggregate, nonessential for T7 viability and that our models for the functions encoded by elements are sufficient. To test our initial design, we replaced the left 11 515 base pairs (bp) of the 39 937 bp wild-type genome with 12 179 bp of engineered DNA. The resulting chimeric genome encodes a viable bacteriophage that appears to maintain key features of the original while being simpler to model and easier to manipulate. The viability of our initial design suggests that the genomes encoding natural biological systems can be systematically redesigned and built anew in service of scientific understanding or human intention.
Molecular Systems Biology 13 September 2005; doi:10.1038/msb4100025
Subject Categories: synthetic biology

Combining two genomes in one cell: Stable cloning of the *Synechocystis* PCC6803 genome in the *Bacillus subtilis* 168 genome

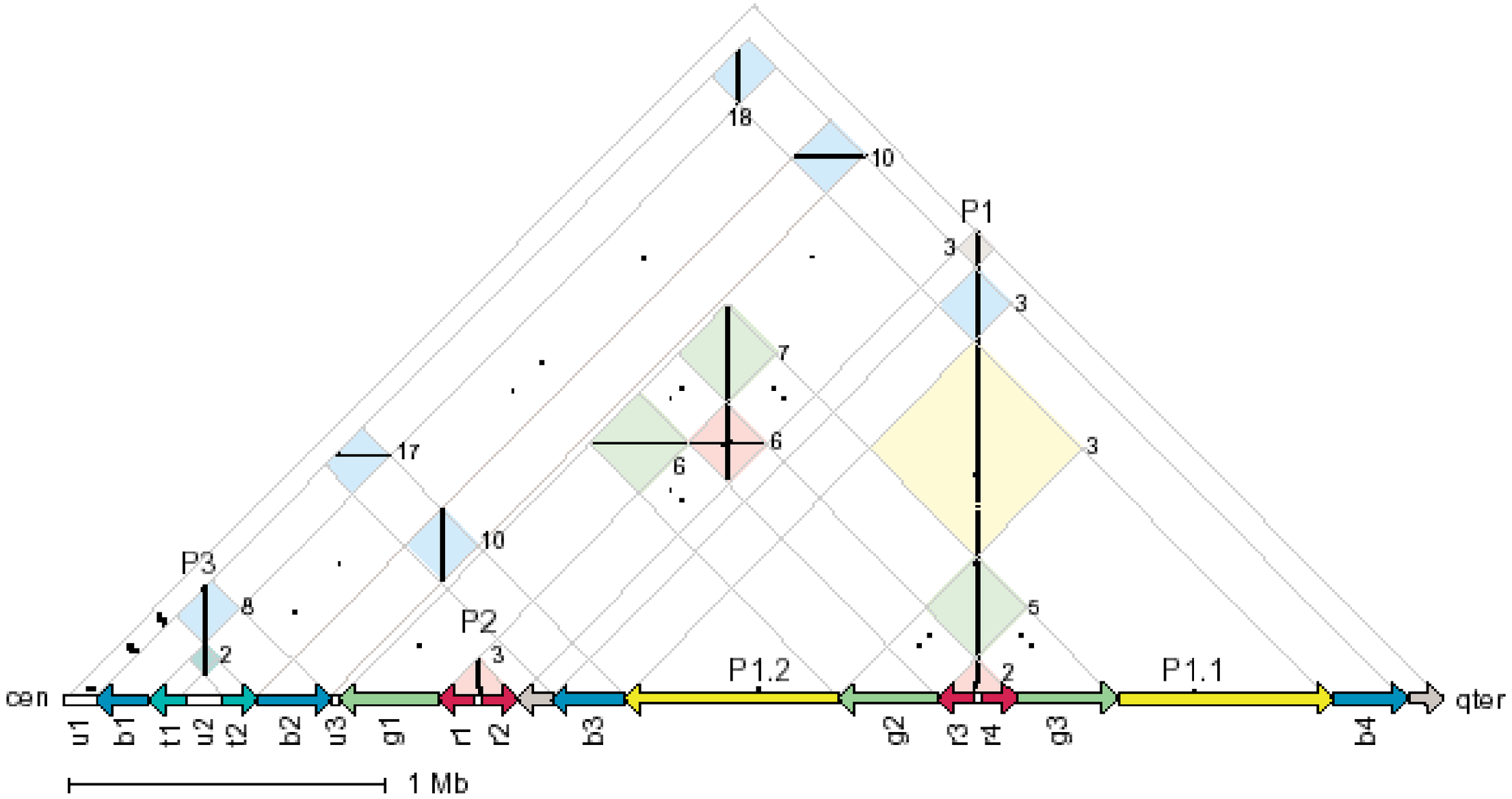
Mitsuhiro Itaya*, Kenji Tsuge, Maki Koizumi, and Kyoko Fujita

Mitsubishi Kagaku Institute of Life Sciences, 11 Minamiooya, Machida-shi, Tokyo 194-8511, Japan

Edited by J. Craig Venter, The J. Craig Venter Institute, Rockville, MD, and approved September 16, 2005 (received for review May 10, 2005)

Cloning the whole 3.5-megabase (Mb) genome of the photosynthetic bacterium *Synechocystis* PCC6803 into the 4.2-Mb genome of the mesophilic bacterium *Bacillus subtilis* 168 resulted in a 7.7-Mb composite genome. We succeeded in such unprecedented large-size cloning by progressively assembling and editing contiguous DNA regions that cover the entire *Synechocystis* genome. The strain containing the two sets of genome grew only in the *B. subtilis* culture medium where all of the cloning procedures were carried out. The high structural stability of the cloned *Synechocystis* genome was closely associated with the symmetry of the bacterial genome structure of the DNA replication origin (*oriC*) and its termination (*terC*) and the exclusivity of *Synechocystis* ribosomal RNA operon genes (*rrnA* and *rrnB*). Given the significant diversity in genome structure observed upon horizontal DNA transfer in nature, our stable laboratory-generated composite genome raised fundamental questions concerning two complete genomes in one cell. Our megasize DNA cloning method, designated megacloning, may be generally applicable to other genomes or genome loci of free-living organisms.

and demonstrated the successful reconstruction of long contiguous DNAs (12–14). Our cloning principle took advantage of features inherent to this bacterium, i.e., the development of natural competence and the subsequent homologous recombination activity in the cytoplasm. Both features are induced because of their association with growth-phase transition (15, 16). The target DNA is guided in the BGM vector by simultaneous homologous recombination at two small flanking DNAs called landing pad sequences (LPS), integrated at the BGM cloning locus before cloning. The two LPS, ordered and oriented correctly, are termed the LPS array (LPA) (13, 14). Sliding the LPA results in elongation of the adjacent target DNA (Fig. 1). We offer such elongation-coupled cloning in the BGM vector, hereafter called inchworm elongation (IWe), as an elegant alternative to current cloning methods. We applied this method in the complete cloning of the whole 3.5-Mb genome of the photosynthetic bacterium *Synechocystis* PCC6803 (17) into the 4.2-Mb genome of the mesophilic bacterium *B. subtilis* 168 (Fig. 2).



Kuroda-Kawaguchi et al., Nature Genetics 29:279 (2001)

Thank you!